Combining existing information from the Pig Industry to identify risk factors for pig diseases.

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Introduction - Background

In the recent years the proactive dynamism of the British Pig Industry led to the implementation of Farm Assurance and Health Schemes.
These schemes collect a vast amount of farm and pig health information suitable for epidemiological analysis. Fig. 1 shows the geographical distribution of the farm members of the schemes.

This Defra funded project aims to use this existing information for epidemiological analysis to identify management practises that predispose pigs for health problems and high Salmonella scores. Fig. 2 highlights the flow diagram of this project.

The results from this study will advise on ways to improve data collection by the various schemes and will show the pig industry how this routinely collected information can be analysed, and possibly updated on a regular basis.

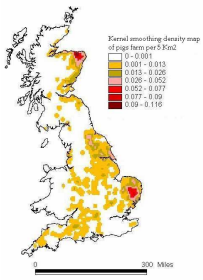

Fig 1: Map representing the geographical distribution of the density of participating farms.

Data Source

We merged data from three major Quality Assurance Schemes in Great Britain with the information from Pig Health Schemes:

Assured British Pigs (ABP), Genesis QA (GQA) and Quality Meat Scotland (QMS).
These databases compile management and structural information from assured premises. Pigs stocking levels; practices for feeding; housing systems; production indoors or outdoors is commonly available from the three schemes.

Methods

- We examine the information available in the Farm Assurance datasets to identify common factors present in the three databases that can be employed as epidemiological inputs.
- We evaluate the consistency of the abattoir lesion scoring to identify the characteristics of the assessment as a diagnostic test (Sensitivity and Specificity).
  We explored the time trend and seasonality patterns of the different lesions. See Fig. 3 and Fig. 4.
- We investigate the spatial distribution of the prevalence for the lesions.
- We use multivariate techniques to evaluate the associations among the different lesions and ZAP- scores.

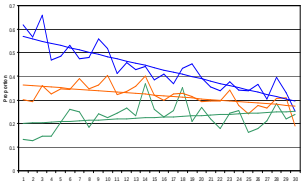

Fig 3: Time trend of the prevalence of Enzootic pneumonia-like lesions in three different groups of herds. Those starting with the lowest prevalence (green); herds staring with highest prevalence (blue) and overall evolution of all the herds together (orange). BPHS data July 2005-December 2007.

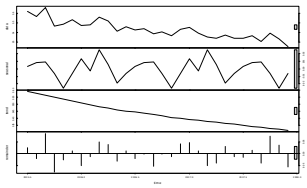

Fig 4: Time Series investigation for Enzootic pneumonia-like lesions. From top to bottom: Data outline; seasonal decomposition; overall trend; remainder. BPHS data July 2005-December 2007.

- We use Generalized Linear Mixed Models: This approach allows accounting for random error due to the three hierarchical clustering scenarios: Company, Farm and Batch level, also allowing for seasonality effects
- A steering committee comprising by pig experts from University, Pig Industry and Government and representatives from the participating Schemes acts as an advisory body regulating the progress of the project.

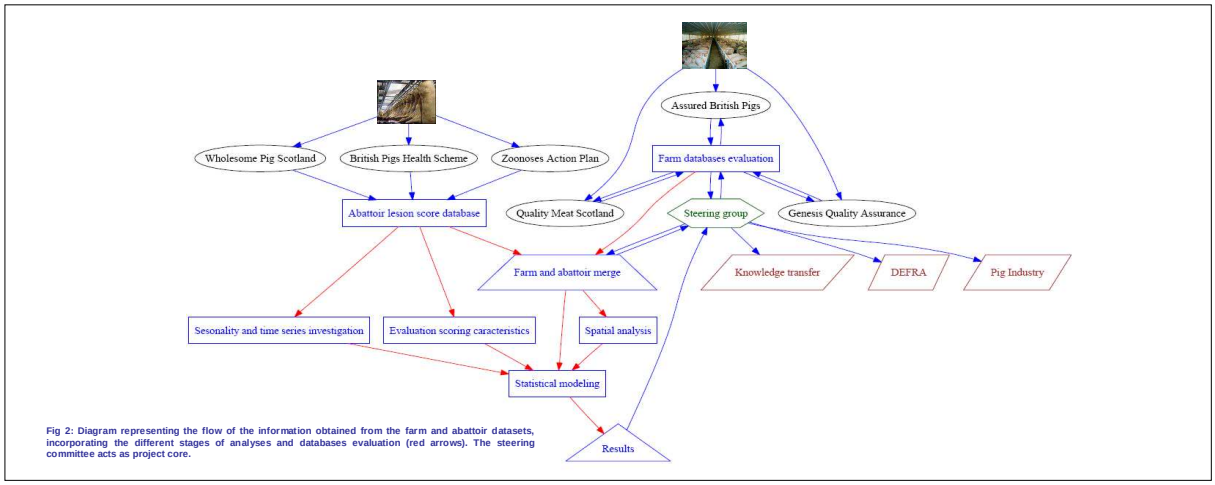

Fig 2: Diagram representing the flow of the information obtained from the farm and abattoir datasets, incorporating the different stages of analyses and databases evaluation (red arrows). The steering committee acts as project core.

Data Source (continued)

Herd Health Schemes collect veterinary abattoir lesion scoring. Wholesome Pigs Scotland (WPS) and British Pig Health Scheme (BPHS) provide routine information on the presence of twelve different lesions generally associated with the occurrence of subclinical disease:

- Enzootic pneumonia
- Pleurisy
- Milk spots
- Hepatic scarring
- Abscess
- Papular dermatitis
- Peritonitis
- Pleuropneumonia
- Pyaemia
- Pericarditis
- Tail biting
- Viral-like pneumonia

Zoonoses Action Plan (ZAP) Salmonella Monitoring Program is based on ELISA testing on meat-juice from samples collected at the abattoirs. Its aim is to identify those farms where high proportions of pigs test positive for Salmonella antibodies.

Preliminary Results - Discussion

Preliminary results based on 647 farms and 2900 batches of pigs suggest that feeding information and pig stocking levels are the principal variables to help in the estimation of the herd prevalence of the different disease conditions.
Allowing for random error at batch level provides the best fit to the data. This fact could be suggesting that batch specific information, e.g. pigs' origin; treatment and vaccination history not currently available in the data sets could be of great value to predict the occurrence of the different conditions.

Acknowledgements

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